SEIAS-SEI model on asymptomatic and super infection malaria with imperfect vaccination

by Muhammad Abdy

Submission date: 03-Jul-2021 11:16AM (UTC+0700)
Submission ID: 1615178904
File name: matic_and_super_infection_Malaria_with_Imperfect_Vaccination.pdf (658.02K)
Word count: 2245
Character count: 11706

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H Maryam[1], M Abdy[2], Alimuddin[2], and S Side[2]

[1]Student of Magister Mathematics, Universitas Negeri Makassar
[2]Department of Mathematics, Faculty of Mathematics and Natural Science, Universitas Negeri Makassar

*Corresponding Author: Syafruddin@unm.ac.id

Abstract. The aims of this research are to build a model of SEIAS-SEI on the spread of malaria; analysing the model; and conducting simulations to predict the number of cases of malaria in disease-free and endemic cases. This research is a theoretical study. This model uses suspected, exposed, infected and acute compartments. Analysis of the model using the matrix generation method, the data used in the simulation is an assumption data to cover the disease-free and endemic malaria cases and the model simulation using Maple. The results obtained are models of SEIRS-SEI in malaria deployments; model analysis generates equilibrium points and basic reproductive numbers to determine the status of malaria deployments in a region. Simulated results provide a sense of the difference between disease-free State and endemic is that there is a decrease in the number of infected and asymptomatic individual groups. In endemic cases, a decrease in the number of infected and asymptomatic individual groups in malaria spread takes a long time. In contrast to disease-free cases, a decline in the number of infected and asymptomatic individuals may take a short time.

1. Introduction

Malaria is a disease caused by parasitic infections of the female Anopheles mosquito genus Plasmodium. Malaria can be transmitted through infected mosquito bites, blood transfusions, syringe, or congenital and is a very deadly disease for human beings [1]. World Malaria Report 2015 mentions that Malaria has invaded 106 countries in the world [2]. The malaria condition in Indonesia shown that there are still 10.7 million inhabitants living in the middle and high endemic areas of malaria. The area mainly includes Papua, West Papua, and NTT. Based on data on 2017, from the number of 514 districts/cities in Indonesia, 266 (52%) Including malaria-free territories, 172 districts /cities (33%) Low endemic, 37 districts/cities (7%) and 39 districts/cities (8%) High endemic [3].

Mathematical modeling of dengue fever, tuberculosis and Malaria has been conducted by [1;4-14]. The study was conducted to predict the number of cases of the disease. The research conducted by [1;9-14] on malaria transmission assumes that malaria sufferers who have recovered become immune and also do not include asymptomatic infection classes, then the mathematical model for the transmission of malaria disease [15] illustrates the math model of SIS-SI in spreading malaria disease with human vaccinations assuming that the human being healed can be infected with an imperfect vaccine induced disease. Furthermore, [1] discusses the SEIRS-SEI type of malaria mathematical model with human treatment, vaccination treatment and treatment. In addition, [14] discusses the SEIARS-SEI mathematical model in malaria disease with asymptomatic and super infection influence to measure the

sensitivity level of the spread of malaria to asymptomatic infection parameters. This research builds the SEIAS-SEI model on Malaria spread, analysis and simulation on the malaria transmission taking into consideration that the sufferer of the malaria can return to suspect and incorporate asymptomatic infected variables into the model.

2. Research Method

The type of research used is theoretical and applied research, which is research examining its theories and applications on the spread of Malaria. The stage of this research is building the SEIAS-SEI model in the transmission of malaria; this model uses suspected, exposed, infected and acute compartments. Model analysis uses the matrix generation method [10], the data used in the simulation is the assumption data to cover disease-free and endemic malaria cases. Model simulation uses Maple to predict the number of malaria cases on the Status of free-disease and endemic.

3. Results and Discussion

3.1. SEIAS-SEI Model for Malaria Transmission

Population changes in the SEIAS-SEI model for Malaria transmission interpreted in Figure 1 and the definition of variables and parameters models presented in Table 1.

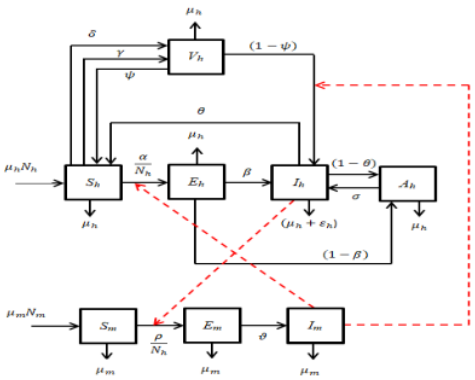

Figure 1. SEIAS-SEI Model flow chart on malaria transmission

Table 1. Definition of SEIAS-SEI Model variables and parameters on Malaria transmission

Variable/Parameter	Definition
S_h	The number of Suspected individuals in population
E_h	The number of Exposed individuals in population
I_h	The number of Infected individuals in population
A_h	The number of Asymptomatic Infected individuals in population
V_h	The number of Vaccine individuals in population
S_m	The number of Suspected mosquitoes
E_m	The number of Exposed mosquitoes
I_m	The number of Infected mosquitoes
N_h	The rate of human birth
α	The rate of infection in humans
ψ	Rate of individuals with vaccine efficacy
$(1-\psi)$	Rate of individuals with vaccine failure in humans
γ	The rate of individual vaccine
δ	The rate of individuals given the However vaccine was ever infected
β	The rate of human displacement is exposed to human

Variable/Parameter	Definition
$(1-\beta)$	The rate of human displacement is exposed to human infected but not detected (*asymptomatic infected*).
σ	Super-Infected constants of infected but undetectable individuals (*asymptomatic infected*).
θ	Human recovered rate constants of malaria parasites
$(1-\theta)$	Displacement rates from infected individuals to asymptomatic population
μ_h	Human mortality rate Naturally
ε_h	Human mortality rate due to malaria
N_m	The rate of Mosquitoes birth
ρ	Rate of infection (mosquito bite level healthy bite infected individuals)
ϑ	Rate of displacement of mosquitoes exposed to infected mosquitoes
μ_m	Constant rate of mosquito death naturally

Based on Figure 1, obtained the SEIAS-SEI model for Malaria transmission disease in Equation (1)–(8), namely:

$$\frac{dS_h}{dt} = \mu_h N_h + \theta I_h + \psi V_h - \left(\delta + \gamma + \mu_h + \frac{\alpha}{N_h} I_m\right) S_h \tag{1}$$

$$\frac{dE_h}{dt} = \frac{\alpha}{N_h} I_m S_h - (1+\mu_h) E_h, \tag{2}$$

$$\frac{dI_h}{dt} = (1-\psi) I_m V_h + \beta E_h + \sigma A_h - (1+\mu_h+\varepsilon_h) I_h \tag{3}$$

$$\frac{dA_h}{dt} = (1-\theta) I_h + (1-\beta) E_h - (\sigma+\mu_h) A_h, \tag{4}$$

$$\frac{dV_h}{dt} = (\delta+\gamma) S_h - (\psi + (1-\psi) I_m + \mu_h) V_h \tag{5}$$

$$\frac{dS_m}{dt} = \mu_m N_m - \left(\frac{\rho}{N_h} I_h + \mu_m\right) S_m \tag{6}$$

$$\frac{dE_m}{dt} = \frac{\rho}{N_h} I_h S_m - (\vartheta + \mu_m) E_m, \tag{7}$$

$$\frac{dI_m}{dt} = \vartheta E_m - \mu_m I_m, \tag{8}$$

3.2. Analysis of SEIAS-SEI Model on Malaria transmission

There are two equilibrium points that are disease-free and endemic equilibrium point. Disease-free equilibrium points shown in equations (9) and (10), while the equilibrium point is endemic to the equation (11) and (12).

$$S^*_h = \frac{\mu_h N_h (\psi + \mu_h)}{(\mu_h)(\psi + \delta + \gamma + \mu_h)}, E_h^* = 0, I_h^* = 0, A_h^* = 0 \text{ and } V^*_h = \frac{\mu_h N_h (\delta+\gamma)}{(\mu_h)(\psi+\delta+\gamma+\mu_h)} \tag{9}$$

$$\mathrm{S}^*_{\mathrm{m}} = \frac{\mathrm{N_m}}{\mu_m}, \ \mathrm{E}^*_{\mathrm{m}} = 0, \text{ and } \mathrm{I}^*_{\mathrm{m}} = 0 \tag{10}$$

$$S_h^{**} = \frac{c_1 N_h}{c_3 c_1 - c_2 - c_1 q_2 \theta}, E_h^{**} = \frac{r_{h1} c_1 N_h}{(c_3 c_1 - c_2 - c_1 q_2 \theta) c}, I_h^{**} = \frac{q_2 c_1 N_h}{c_3 c_1 - c_2 - c_1 q_2 \theta}, \quad A_h^{**} = \frac{q_1 c_1 N_h}{c_3 c_1 - c_2 - c_1 q_2 \theta} \text{ and}$$

$$V_h^{**} = \frac{c_5 c_1 N_h}{(c_3 c_1 - c_2 - c_1 q_2 \theta) c_1}, \tag{11}$$

$$S_m^{**} = \frac{\mu_m N_m}{r_m + \mu_m}, E_m^{**} = \frac{r_m \mu_m N_m}{(r_m + \mu_m)(\vartheta + \mu_m)} \text{ and } I_m^{**} = \frac{\vartheta r_m N_m}{(r_m + \mu_m)(\vartheta + \mu_m)} \quad (12)$$

With,

$$b = \frac{\alpha}{N_h}, \quad c = 1 + \mu_h, \quad g = 1 - \psi, \quad k = 1 + \mu_h + \varepsilon_h,$$

$$q = 1 - \theta, \quad t = 1 - \beta, \quad x = \sigma + \mu_h, \quad y = \frac{\rho}{N_h}, \quad z = \vartheta + \mu_m, \; r_{h1} = \frac{\alpha}{N_h} I_m, \; r_{h2} = (1 - \psi) I_m, r_m = \frac{\rho}{N_h} I_h,$$

$$c_3 = \delta + \gamma + \mu_h + r_{h1}, \; c_1 = \psi + r_{h2} + \mu_h \;\; c_2 = \psi(\delta + \gamma), a_1 = \frac{q r_{h2}}{kx - q}, \;\; a_2 = \frac{(q\beta + kt)}{kx - q},$$

$$q_1 = \frac{(a_1 cc_5 + a_2 c_1 r_{h1})}{cc_1}, \quad q_2 = \frac{r_{h2} cc_5 + \beta c_1 r_{h1} + cc_1 q_1 \sigma}{cc_1 c_4},$$

3.3. The Basic Reproduction Number of SEIAS-SEI Model on Malaria Transmission

Thus obtained the basic reproduction number R_0 namely:

$$R_0 = \sqrt{\frac{bxyN_h N_m (\psi + \mu_h)}{\mu_m (kx - q\sigma)(\psi + \delta + \gamma + \mu_h)}} \quad (13)$$

The basic reproduction number is an epidemic threshold value that will be the benchmark rate of malaria spread in the population. If $R_0 \leq 1$, then the number of infected individuals will decline in each generation, so the disease will disappear and if $R_0 > 1$, then the number of infected individuals will increase in each generation, so that the disease will increase and endemic.

3.4. Simulation Result of SEIAS-SEI Models for Malaria Transmission Free Cases

Simulation Results of The combined graph of the overall comparison of the SEIAS-SEI model compartment in cases of malaria disease seen in Figure 2.

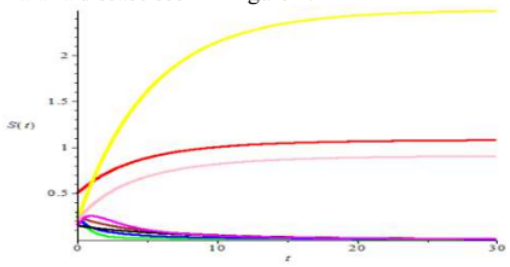

Figure 2. Combined SEIS-SEI model variables for Malaria disease free cases

Based on Figure 2 it seen that the number of vulnerable individual's increases rapidly from the first year then begins to decline in the 14th year. The change in the number of individuals exposed decreases drastically from the first year. Then the number of infected individuals decreases drastically from the first year to around the 8th year. The change in the number of asymptomatic individuals increased rapidly from the first year to the 3rd year then began to decline drastically from the 4th year. Then the amount of vaccine individuals increased rapidly from the first year then began to decline in the 10th year. Then that the number of suspected Mosquitoes increases rapidly from the first year then begins to decline in the 10th year.

3.5. Simulation Result of SEIAS-SEI Models for Malaria Endemic Cases

Simulated results of Endemic cases of malaria disease seen in Figure 3.

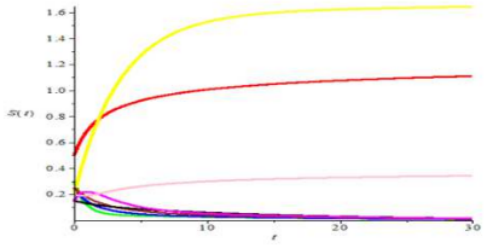

Figure 3. Combined SEIS-SEI model variables for Malaria endemic cases

Based on Figure 3, it can be seen that the number of suspected individuals increased rapidly from the first year then began to decline in the 10th year. The change in the number of individuals exposed decreases drastically since the first year. Then the number of infected individuals decreases drastically in the first year to the 8th year. The change in the number of asyimptomatic individuals increased rapidly from the first year to the 3rd year, then began to decline drastically in the 4th year. Then that the amount of vaccine individuals increased rapidly in the first year then began to decline in the 10th year. Then that the number of virus carrier mosquitoes has decreased since the first year

3.6. Discussion

A study on malaria conducted by [1] discusses the SEIRS-SEI type malaria mathematical model with human treatment, vaccination treatment and treatment. Then the research results [11] are models of SEIARS-SEI mathematics in malaria disease with asymptomatic and super infection influence to measure the sensitivity level of the spread of malaria against asymptomatic infection parameters. This research produces the SEIAS-SEI model on Malaria deployments, analysis and simulation on the transmission of malaria by considering that malaria sufferers who have recovered can return to suspect and also incorporate asymptomatic infected variables into the model, the SEIAS-SEI model on the study resulted in analysis and simulation on disease free cases and endemic Malaria which suggests that in endemic cases, it takes a long time to reduce the number of malaria infected populations.

4. Conclusion

Based on the results obtained, it can be concluded that: Malaria transmission can be presented in a mathematical model of SEIAS-SEI; Model analysis gives an overview of the stimulating point of malaria transmission, meaning that malaria disease persists in that amount. The basic reproduction number gives a description of the state of malaria infection in a region of disease-free status or endemic malaria. Simulated results provide an overview of the predicted number of cases of malaria in a region, so the government is in early prevention.

Acknowledgements

We would like thank to Dikti No:052/SP2H/LT/DRPM/2020 for financial support.

References

[1] Resmawan and Nurwan 2017 *J. Mat. Integr*. **13** (2) 105
[2] Ministry of Health Indonesia 2018 *World Malaria Day, Government Expands Malaria Free Areas.* http://www.depkes.go.id/article/view/18043000010/hari-malaria-sedunia-pemerintah-perluas-wilayah-bebas-malaria.html
[3] Kemenkes RI 2016 *Infodat in Malaria* http://www.depkes.go.id/article/view/16090700001/infodatin-malaria.html
[4] Syafruddin, S and M.S.M Noorani 2013 *Int. J. Simul. Process Model. (IJSPM)* **8**(2/3) 177
[5] Syafruddin, S and M.S.M Noorani 2013 *World J. Model. Simul*. **9**(2) 96
[6] Syafruddin, S 2015 *Adv. Sci. Lett.* **21** (2) 137

[7] Riska Y F And Bobby P 2019 *Mater. Sci. Forum*. **967** 3
[8] Laarabi H, Labriji EH, Rachik M, Kaddar A 2012 *Model. Control*. **17**(4) 448459
[9] Abdullahi MB, Hasan YA, Abdullah FA 2013 *Appl. Math. Sci.* **7** (62) 30793095
[10] Laarabi H, Labriji EH, Rachik M, Kaddar A 2012 *Model. Control*. **17**(4) 448459
[11] Laneri K 2015 In *Proceedings of the National Academy of Sciences* **112**(28) 8786
[12] Roy M 2015 *Malaria J.* **14**(1) 1
[13] Safan M and Rihan FA 2014 *Math. Comput. Simul.* **96** 195
[14] Stella Maryana Belwawin 2019 *Enferm. Clin.* **30** 516
[15] N. Fajri, P. Sianturi, and T. Bakhtiar 2016 *J. Manaj. Agribisnis* **15**(2) 51

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